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============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=7; day=18; hr=10; min=21; sec=55; ms=345; ]
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Application No: 10581761   Version No: 2.0

Input Set:

Output Set:

Started: 2008-07-17 17:01:45.584
Finished: 2008-07-17 17:01:48.344
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 760 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 52
Actual SeqID Count: 52

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Validated organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)

Input Set:

Output Set:

Started:	2008-07-17 17:01:45.584
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Actual SeqID Count:	52

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<210> 1
<211> 736
<212> DNA
<213> Murinae

<400> 1
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tccgctcggg ccagacttgc taccatccca ttcgcgggga ccagctggct ctgctggggc 180
gcaggactta tcctcggccg catgagtacc tgtccccagc ggatctcccc aagaattggg 240
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tcaagaggaa aggtgcatgg ccctccatcc tgctgtccgt acagaatgtc attgactgtg 420
gcaatgctgg ctcttgtgaa gggggcaatg accttccggt gtgggagtat gcccacaagc 480
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taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga attacaccct 600
ctggagagtg ggtgattacg gtccctgtcc gggagggaga agatgatggc gagatctatg 660
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<210> 2
<211> 1404
<212> DNA
<213> Murinae

<400> 2
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<210> 3
<211> 306
<212> PRT
<213> Murinae


<400> 3
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            20                  25                  30
Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly
        35                  40                  45
Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu
    50                  55                  60
Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser
65                  70                  75                  80
Val Thr Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala
                85                  90                  95
His Gly Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys
            100                 105                 110
Gly Ala Trp Pro Ser Ile Leu Leu Ser Val Gln Asn Val Ile Asp Cys
        115                 120                 125
Gly Asn Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Pro Val Trp Glu
    130                 135                 140
Tyr Ala His Lys His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln
145                 150                 155                 160
Ala Lys Asp Gln Asp Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Thr
                165                 170                 175
Glu Phe Lys Glu Cys His Thr Ile Gln Asn Tyr Thr Leu Trp Arg Val
            180                 185                 190
Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile
        195                 200                 205
Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met
```

```
             210                 215                 220
Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val
225                 230                 235                 240
Ile Asn His Ile Ile Ser Val Ala Gly Trp Gly Val Ser Asn Asp Gly
                245                 250                 255
Ile Glu Tyr Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu
                260                 265                 270
Lys Gly Trp Met Arg Ile Val Thr Ser Thr Tyr Lys Gly Gly Thr Gly
            275                 280                 285
Asp Ser Tyr Asn Leu Ala Ile Glu Ser Ala Cys Thr Phe Gly Asp Pro
        290                 295                 300
Ile Val
305
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<400> 4

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caggtggcg gccgcttctg ctgctcgtgc tgctggcggg cgcggcgcag gcgggcctct 180
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gcggtaacgc tggctcctgt gaagggggta atgacctgtc cgtgtgggac tacgcccacc 540
agcacggcat ccctgacgag acctgcaaca actaccaggc caaggaccag gagtgtgaca 600
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Leu Ala Gly Ala Ala Gln Gly Gly Leu Tyr Phe Arg Arg Gly Gln Thr
                20                  25                  30
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         35                  40                  45
Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
      50                  55                  60
Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr
65                  70                  75                  80
Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala
                 85                  90                  95
Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala
              100                 105                 110
Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn
         115                 120                 125
Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala
      130                 135                 140
His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys
145                 150                 155                 160
Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe
              165                 170                 175
Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp
              180                 185                 190
Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala
         195                 200                 205
Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn
      210                 215                 220
Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn
225                 230                 235                 240
His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr
              245                 250                 255
Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp
              260                 265                 270
Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr
         275                 280                 285
Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val
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<211> 646
<212> DNA
<213> Murinae

<400> 6
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tttaccaaga ctctttcggg actttcacca tcaatgaatc cagtatagct gattctccaa  180
gattccctca tagaggaatt ttaattgata catctagaca cttcctgcct gtgaagacaa  240
ttttaaaaac tctggatgcc atggctttta ataagtttaa tgttcttcac tggcacatag  300
tggacgacca gtctttccct tatcagagta ccacttttcc tgagctaagc aataagggaa  360
gctactcttt gtctcatgtc tatacaccaa cgatgtccg gatggtgctg gagtacgccc  420
ggctccgagg gattcgagtc ataccagaat ttgataccc tggccataca cagtcttggg  480
gcaaaggaca gaaaaacctt ctaactccat gttacaatca aaaaactaaa actcaagtgt  540
ttgggcctgt agacccaact gtaaacacaa cgtatgcatt ctttaacaca ttttttcaaag  600
aaatcagcag tgtgtttcca gatcagttca tccacttggg aggaga                  646
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<210> 7
<211> 1805
<212> DNA
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<213> Murinae

<400> 7
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gctggtgtcg ctagtgtcgc tggccctagt ggccccggcc cgactgcaac ctgcgctatg 180
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gtttcggcga tattacaact atgtttttgg tttctacaag agacatcatg gccctgctag 360
atttcgagct gagccacagt tgcagaagct cctggtctcc attaccctcg agtcagagtg 420
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tttct 1805

<210> 8
<211> 536
<212> PRT
<213> Murinae

<400> 8
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            20   25   30

Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu
        35   40   45

Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser
    50   55   60

Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr
65   70   75   80

Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg
                85   90   95

Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu
            100   105   110

Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr
            115   120   125

Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val
    130   135   140
Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln
145   150   155   160
Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser
                165   170   175
Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe
                180   185   190
Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn
            195   200   205
Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro
    210   215   220
Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser
225   230   235   240
Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr
                245   250   255
Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly
            260   265   270
His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys
            275   280   285
Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr
    290   295   300
Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser
305   310   315   320
Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu
                325   330   335
Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg
            340   345   350
Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys
            355   360   365
Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp
    370   375   380
Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val
385   390   395   400
Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr
                405   410   415
Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu
            420   425   430
Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu
    435   440   445
Asn Phe Glu Gly Ser Glu Lys Gln Lys Gln Leu Val Ile Gly Gly Glu
    450   455   460
Ala Cys Leu Trp Gly Glu Phe Val Asp Ala Thr Asn Leu Thr Pro Arg
465   470   475   480
Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg Leu Trp Ser Pro Lys
                485   490   495
Thr Val Thr Asp Leu Glu Asn Ala Tyr Lys Arg Leu Ala Val His Arg
                500   505   510
Cys Arg Met Val Ser Arg Gly Ile Ala Ala Gln Pro Leu Tyr Thr Gly
            515   520   525
Tyr Cys Asn Tyr Glu Asn Lys Ile
    530   535

<210> 9
<211> 1746
<212> DNA

<213> Homo sapiens

<400> 9
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